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SEQUENCE LISTING

<110> Igawa, Tomoyuki
Sekimori, Yasuo

<120> IgM high concentration stabilized solution

<130> 14875-159US1

<150> PCT/JP2004/14935
2004-10-08

<150> JP 2003-351388

<151> 2003-10-09

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1779)

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gtc	cag	tgt	gag	gtg	cag	ctg	ttg	gat	tct	ggg	gga	ggc	ttg	gta	cag	96
Val	Gln	Cys	Glu	Val	Gln	Leu	Leu	Asp	Ser	Gly	Gly	Gly	Leu	Val	Gln	
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cct	ggg	ggg	tgc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttt	144
Pro	Gly	Gly	Cys	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	
		35					40					45				

agc	agc	tgt	gcc	atg	agc	tgg	gtc	cgc	cag	gct	cca	ggg	aag	ggg	ctg	192
Ser	Ser	Cys	Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
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gag	tgg	gtc	tca	gct	att	agt	ggg	agt	ggg	ggg	agc	aca	tac	tac	gca	240
Glu	Trp	Val	Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	
65					70					75					80	

gac	tcc	gtg	aag	ggc	cgg	ttc	acc	atc	tcc	aga	gac	aaa	tcc	aag	aac	288
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Lys	Ser	Lys	Asn	
				85					90					95		

acg	ttg	tat	ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gcc	gta	336
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	
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Tyr	Tyr	Cys	Ala	Lys	Gly	Gly	Asn	Asp	Ile	Leu	Thr	Gly	Tyr	Tyr	Ala	
		115					120					125				
tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca	ggg	agt	gca	tcc	gcc	432
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	Ala	Ser	Ala	
	130					135					140					
cca	acc	ctt	ttc	ccc	ctc	gtc	tcc	tgt	gag	aat	tcc	ccg	tcg	gat	acg	480
Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn	Ser	Pro	Ser	Asp	Thr	
	145				150					155					160	
agc	agc	gtg	gcc	gtt	ggc	tgc	ctc	gca	cag	gac	ttc	ctt	ccc	gac	tcc	528
Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp	Phe	Leu	Pro	Asp	Ser	
			165						170					175		
atc	act	ttc	tcc	tgg	aaa	tac	aag	aac	aac	tct	gac	atc	agc	agc	acc	576
Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser	Asp	Ile	Ser	Ser	Thr	
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cgg	ggc	ttc	cca	tca	gtc	ctg	aga	ggg	ggc	aag	tac	gca	gcc	acc	tca	624
Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys	Tyr	Ala	Ala	Thr	Ser	
		195					200					205				
cag	gtg	ctg	ctg	cct	tcc	aag	gac	gtc	atg	cag	ggc	aca	gac	gaa	cac	672
Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln	Gly	Thr	Asp	Glu	His	
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gtg	gtg	tgc	aaa	gtc	cag	cac	ccc	aac	ggc	aac	aaa	gaa	aag	aac	gtg	720
Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	Lys	Asn	Val	
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cct	ctt	cca	gtg	att	gct	gag	ctg	cct	ccc	aaa	gtg	agc	gtc	ttc	gtc	768
Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	Val	Phe	Val	
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cca	ccc	cgc	gac	ggc	ttc	ttc	ggc	aac	ccc	cgc	aag	tcc	aag	ctc	atc	816
Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	Lys	Leu	Ile	
			260					265					270			
tgc	cag	gcc	acg	ggg	ttc	agt	ccc	cgg	cag	att	cag	gtg	tcc	tgg	ctg	864
Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	Ser	Trp	Leu	
		275					280					285				
cgc	gag	ggg	aag	cag	gtg	ggg	tct	ggc	gtc	acc	acg	gac	cag	gtg	cag	912
Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	Gln	Val	Gln	
	290					295					300					
gct	gag	gcc	aaa	gag	tct	ggg	ccc	acg	acc	tac	aag	gtg	acc	agc	aca	960
Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	Thr	Ser	Thr	
	305				310					315					320	
ctg	acc	atc	aaa	gag	agc	gac	tgg	ctc	ggc	cag	agc	atg	ttc	acc	tgc	1008
Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Gly	Gln	Ser	Met	Phe	Thr	Cys	
			325						330					335		

cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met 340 345 350	1056
tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro 355 360 365	1104
tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu 370 375 380	1152
gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg 385 390 395 400	1200
cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His 405 410 415	1248
ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp 420 425 430	1296
gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp 435 440 445	1344
ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala 450 455 460	1392
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu 465 470 475 480	1440
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser 485 490 495	1488
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser 500 505 510	1536
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro 515 520 525	1584
ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp 530 535 540	1632
aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro 545 550 555 560	1680
aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc	1728

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
565 570 575

ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac 1776
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tga 1779

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Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
65 70 75 80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
85 90 95
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
115 120 125
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
130 135 140
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
145 150 155 160
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
165 170 175
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
180 185 190
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
195 200 205
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
210 215 220
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
225 230 235 240
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
245 250 255
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
260 265 270
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
275 280 285
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
290 295 300
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
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aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg 65 70 75 80	240
gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp 85 90 95	288
ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr 100 105 110	336
tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr 115 120 125	384
aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe 130 135 140	432
ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys 145 150 155 160	480
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val 165 170 175	528
gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln 180 185 190	576
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser 195 200 205	624
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His 210 215 220	672
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235 240	720
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20          25          30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35          40          45
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50          55          60
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65          70          75          80
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85          90          95
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100         105         110
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
115         120         125
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
130         135         140
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
145         150         155         160
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
165         170         175
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
180         185         190
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
195         200         205
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
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<212> DNA

<213> Homo sapiens

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1          5          10          15

gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac      96
Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
20          25          30

aac aaa tgt aag tgt gcc cgg att act tcc agg atc atc cgt tct tcc      144
Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
35          40          45

gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt      192

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Pro	Leu	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg		
65					70					75				80			
acc	aga	ttt	gtg	tac	cat	ttg	tct	gac	ctc	tgt	aaa	aaa	tgt	gat	cct	288	
Thr	Arg	Phe	Val	Tyr	His	Leu	Ser	Asp	Leu	Cys	Lys	Lys	Cys	Asp	Pro		
				85					90					95			
aca	gaa	gtg	gag	ctg	gat	aat	cag	ata	gtt	act	gct	acc	cag	agc	aat	336	
Thr	Glu	Val	Glu	Leu	Asp	Asn	Gln	Ile	Val	Thr	Ala	Thr	Gln	Ser	Asn		
			100					105					110				
atc	tgt	gat	gaa	gac	agt	gct	aca	gag	acc	tgc	tac	act	tat	gac	aga	384	
Ile	Cys	Asp	Glu	Asp	Ser	Ala	Thr	Glu	Thr	Cys	Tyr	Thr	Tyr	Asp	Arg		
		115					120					125					
aac	aag	tgc	tac	aca	gct	gtg	gtc	cca	ctc	gta	tat	ggg	ggg	gag	acc	432	
Asn	Lys	Cys	Tyr	Thr	Ala	Val	Val	Pro	Leu	Val	Tyr	Gly	Gly	Glu	Thr		
		130				135				140							
aaa	atg	gtg	gaa	aca	gcc	tta	acc	cca	gat	gcc	tgc	tat	cct	gac	taa	480	
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145					150					155							

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Ala	Val	His	Val	Lys	Ala	Gln	Glu	Asp	Glu	Arg	Ile	Val	Leu	Val	Asp		
			20					25					30				
Asn	Lys	Cys	Lys	Cys	Ala	Arg	Ile	Thr	Ser	Arg	Ile	Ile	Arg	Ser	Ser		
		35				40						45					
Glu	Asp	Pro	Asn	Glu	Asp	Ile	Val	Glu	Arg	Asn	Ile	Arg	Ile	Ile	Val		
	50				55					60							
Pro	Leu	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg		
65					70					75				80			
Thr	Arg	Phe	Val	Tyr	His	Leu	Ser	Asp	Leu	Cys	Lys	Lys	Cys	Asp	Pro		
				85					90					95			
Thr	Glu	Val	Glu	Leu	Asp	Asn	Gln	Ile	Val	Thr	Ala	Thr	Gln	Ser	Asn		
			100					105					110				
Ile	Cys	Asp	Glu	Asp	Ser	Ala	Thr	Glu	Thr	Cys	Tyr	Thr	Tyr	Asp	Arg		
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Asn	Lys	Cys	Tyr	Thr	Ala	Val	Val	Pro	Leu	Val	Tyr	Gly	Gly	Glu	Thr		
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<210> 10
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<210> 11
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<210> 16
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24

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28

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26